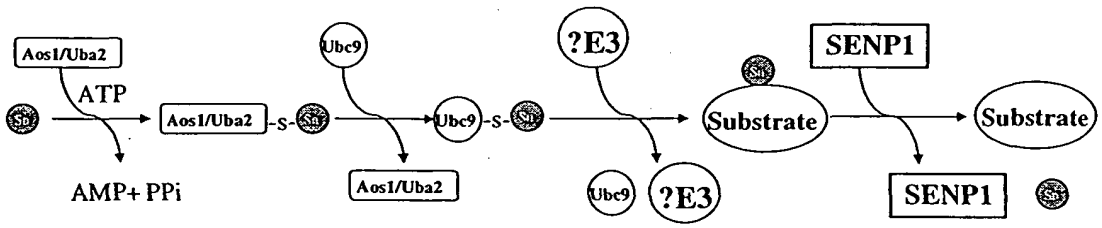


FIG. 1. Sentrinization and de-sentrinization pathway.

FIG. 2

```
1       acctagcgactcttccggtgctgtgaaggcggttccggttcgcggcggttcccgggtttt
61      gcgttccgcgcccggccggaaaccccttcgcatggcagccggttccggttcggactttgt
121     atctttgctaaagtcagtgatgtgaaaagacttgaaatggatgatattgctgataggatg
                                          M  D  D  I  A  D  R  M      8
181     aggatggatgctggagaagtgactttagtgaaccacaactccgtattcaaaacccacctc
        R  M  D  A  G  E  V  T  L  V  N  H  N  S  V  F  K  T  H  L     28
241     ctgccacaaacaggttttccagaggaccagctttcgctttctgaccagcagattttatct
        L  P  Q  T  G  F  P  E  D  Q  L  S  L  S  D  Q  Q  I  L  S     48
301     tccaggcaaggacatttggaccgatcttttacatgttccacaagaagtgcagcttataat
        S  R  Q  G  H  L  D  R  S  F  T  C  S  T  R  S  A  A  Y  N     68
361     ccaagctattactcagataatccttcctcagacagttttcttggctcaggcgatttaaga
        P  S  Y  Y  S  D  N  P  S  S  D  S  F  L  G  S  G  D  L  R     88
421     acctttggccagagtgcaaatggccaatggagaaattctaccccatcgtcaagctcatct
        T  F  G  Q  S  A  N  G  Q  W  R  N  S  T  P  S  S  S  S  S    108
481     ttacaaaaatcaagaaacagccgaagtctttacctcgaaacccgaaagacctcaagtgga
        L  Q  K  S  R  N  S  R  S  L  Y  L  E  T  R  K  T  S  S  G    128
541     ttatcaaacagttttgcgggaaagtcaaaccatcactgccatgtatctgcatatgaaaaa
        L  S  N  S  F  A  G  K  S  N  H  H  C  H  V  S  A  Y  E  K    148
601     tcttttcctattaaacctgttccaagtccatcttggagtggttcatgtcgtcgaagtctt
        S  F  P  I  K  P  V  P  S  P  S  W  S  G  S  C  R  R  S  L    168
661     ttgagccccaagaaaactcagaggcgacatgttagtacagcagaagagacagttcaagaa
        L  S  P  K  K  T  Q  R  R  H  V  S  T  A  E  E  T  V  Q  E    188
721     gaagaaagagagatttacagacagctgctacagatggtcacagggaaacagtttactata
        E  E  R  E  I  Y  R  Q  L  L  Q  M  V  T  G  K  Q  F  T  I    208
781     gccaaacccaccacacatttccttttacacctgtctcgatgtcttagttccagtaaaaat
        A  K  P  T  T  H  F  P  L  H  L  S  R  C  L  S  S  S  K  N    228
841     actttgaaagactcactgtttaaaaatggaaactcttgtgcatctcagatcattggctct
        T  L  K  D  S  L  F  K  N  G  N  S  C  A  S  Q  I  I  G  S    248
901     gatacttcatcatctggatctgccagcattttaactaaccaggaacagctgtcccacagt
        D  T  S  S  S  G  S  A  S  I  L  T  N  Q  E  Q  L  S  H  S    268
961     gtatattccctatcttcttataccccagatgttgcatttggatccaaagattctggtact
        V  Y  S  L  S  S  Y  T  P  D  V  A  F  G  S  K  D  S  G  T    288
1021    cttcatcatccccatcatcaccactctgttccacatcagccagataacttagcagcttca
        L  H  H  P  H  H  H  H  S  V  P  H  Q  P  D  N  L  A  A  S    308
1081    aatacacaatctgaaggatcagactctgtgattttactgaaagtgaaagattcccagact
        N  T  Q  S  E  G  S  D  S  V  I  L  L  K  V  K  D  S  Q  T    328
1141    ccaactcccagttctactttcttccaggcagagctgtggatcaaagaattaactagtgtt
        P  T  P  S  S  T  F  F  Q  A  E  L  W  I  K  E  L  T  S  V    348
1201    tatgattctcgagcacgagaaagattgcgccagattgaagaacagaaggcattggcctta
        Y  D  S  R  A  R  E  R  L  R  Q  I  E  E  Q  K  A  L  A  L    368
1261    cagcttcaaaaccagagattgcaggagcgggaacattcagtacatgattcagtagaacta
        Q  L  Q  N  Q  R  L  Q  E  R  E  H  S  V  H  D  S  V  E  L    388
1321    catcttcgtgtacctcttgaaaaggagattcctgttactgttgtccaagaaacacaaaaa
        H  L  R  V  P  L  E  K  E  I  P  V  T  V  V  Q  E  T  Q  K    408
1381    aaaggtcataaattaactgatagtgaagatgaatttcctgaaattacagaggaaatggag
        K  G  H  K  L  T  D  S  E  D  E  F  P  E  I  T  E  E  M  E    428
1441    aaagaaataaagaatgtatttcgtaatgggaatcaggatgaagttctcagtgaagcattt
        K  E  I  K  N  V  F  R  N  G  N  Q  D  E  V  L  S  E  A  F    448
1501    cgcctgaccattacacgcaaagatattcaaactctaaaccatctgaattggctcaatgat
        R  L  T  I  T  R  K  D  I  Q  T  L  N  H  L  N  W  L  N  D    468
1561    gagatcatcaatttctacatgaatatgctgatggagcgaagtaaagagaagggcttgcca
        E  I  I  N  F  Y  M  N  M  L  M  E  R  S  K  E  K  G  L  P    488
1621    agtgtgcatgcatttaatacctttttcttcactaaattaaaaacggctggttatcaggca
        S  V  H  A  F  N  T  F  F  F  T  K  L  K  T  A  G  Y  Q  A    508
1681    gtgaaacgttggacaaagaaagtagatgtatttctgttgacattcttttggtgcccatt
        V  K  R  W  T  K  K  V  D  V  F  S  V  D  I  L  L  V  P  I    528
1741    cacctgggagtacactggtgtctagctgttgtggactttagaaagaagaatattacctat
        H  L  G  V  H  W  C  L  A  V  V  D  F  R  K  K  N  I  T  Y    548
1801    tacgactccatgggtgggataaacaatgaagcctgcagaatactcttgcaatacctaaag
        Y  D  S  M  G  G  I  N  N  E  A  C  R  I  L  L  Q  Y  L  K    568
1861    caagaaagcattgacaagaaaaggaaagagtttgacaccaatggctggcagcttttcagc
        Q  E  S  I  D  K  K  R  K  E  F  D  T  N  G  W  Q  L  F  S    588
1921    aagaaaagccagattcctcagcagatgaatggaagtgactgtgggatgtttgcctgcaaa
        K  K  S  Q  I  P  Q  Q  M  N  G  S  D  C  G  M  F  A  C  K    608
1981    tatgctgactgtattaccaaagacagaccaatcaacttcacacagcaacacatgccatac
        Y  A  D  C  I  T  K  D  R  P  I  N  F  T  Q  Q  H  M  P  Y    628
2041    ttccggaagcggatggtctgggagatcctccaccgaaaactcttgtgaagactgtctcac
        F  R  K  R  M  V  W  E  I  L  H  R  K  L  L  *                643
2101    ttagcagaccttgaccatgtgggggaccagctctttgttgtctacagccagagaccttgg
2161    aaacagctgctcccagccctctgctgttgtaacacccttgatcctggaccaggccctggc
2221    gagatgcattcacaagcacatctgcctttccttttgtatctcagatactatttttgcaaa
2281    gaaactttggtgctgtgaaaggggtgagggacatccctaagctgaagagagagactgctt
2341    ttcacttcttcagttctgccatcttgttttcaaagggctccagcctcactcagtccctaa
```

2401 ttatgggactgagaaaagcttggaaagaatcttggtttcatataaattcttgtggttagg
2461 Ccttactaagaagtaggaaagggcatgggcaaaaggtagggataaaaaccac

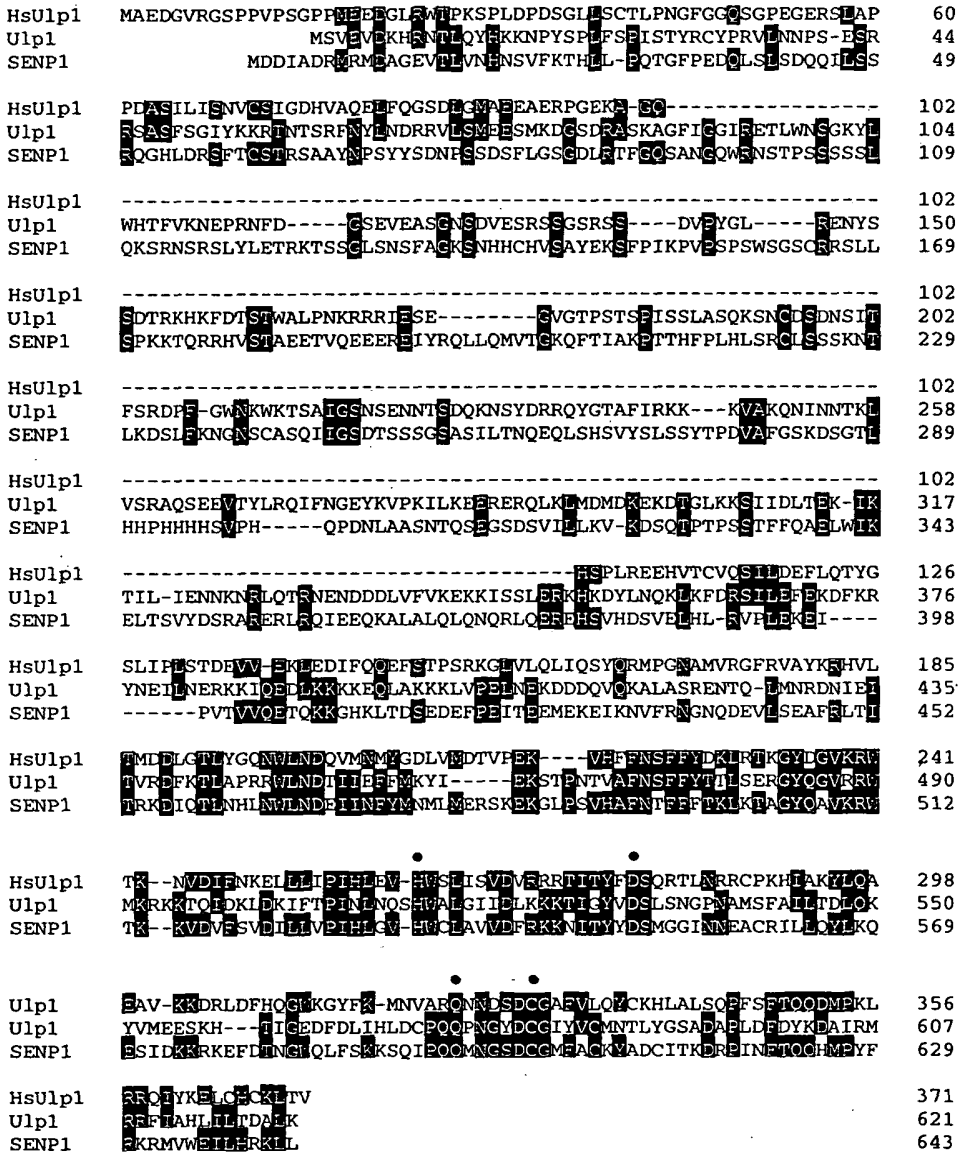


FIG. 3

FIG. 4A.

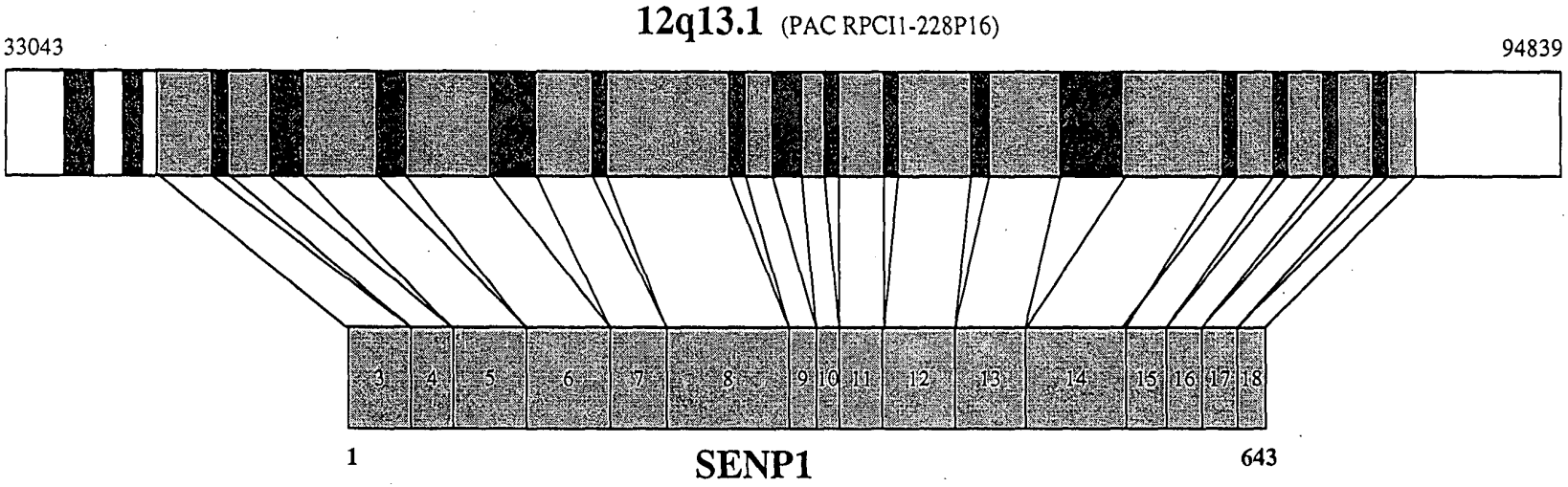


FIG. 4B.

EXON No.	Length (bp)	5'Splice donor	Intron length(kb)	3'Splice acceptor
1	112	GGTTCG GTGAGT	4.4	TTATAG GACTTT
2	47	AAATGG GTAAGA	3.4	CCCCAG ATGATA
3	132	CAGCAG GTTAGG	1.5	GTTTAG ATTTTA
4	85	ACTCAG GTATGA	7.3	TTTTAG ATAATC
5	160	CTCAAG GTTCGT	5.0	TTTTAG TGGATT
6	172	GAAGAG GTAAGG	8.7	TTATAG ACAGTT
7	104	ACACCT GTGAGT	0.08	TGCTAG GTCTCG
8	284	CTGAAG GTAAAC	2.6	TCTTAG GATCAG
9	55	TCCCAG GTAAAC	4.7	CCATAG TTCTAC
10	39	AGAATT GTAAGT	1.2	TTCTAG AACTAG
11	85	AACCAG GTAAAA	0.37	TTTCAG AGATTG
12	156	ACAGAG GTAAGT	1.2	CTCAAG GAAATG
13	132	GATGAG GTAATG	14.4	CCACAG ATCATC
14	204	AGCTGT GTGAGT	0.84	TCTCAG GTTGTG
15	80	ACTCTT GTAAGT	0.94	CTTTAG GCAATA
16	85	AGCCAG GTACCT	0.53	CAGGAG ATTCCT
17	93	ACACAG GTGAGC	0.97	CTACAG CAACAC
18	487			

Fig. 5A

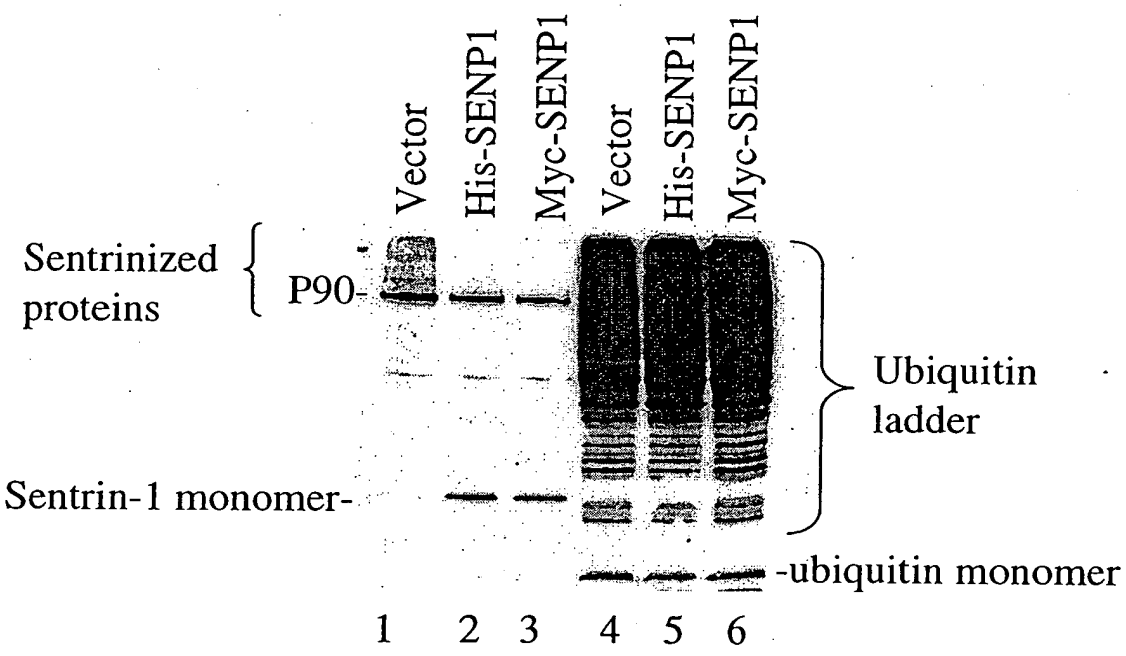
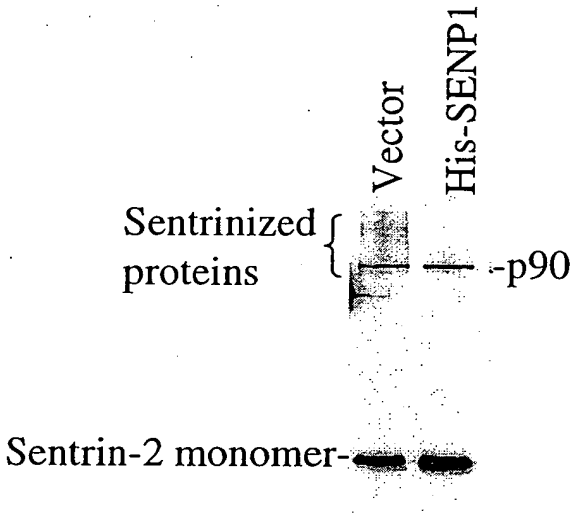

Vector
His-SENP1
Myc-SENP1
Vector
His-SENP1
Myc-SENP1
Sentrinized proteins
P90-
Ubiquitin ladder
Sentrin-1 monomer-
-ubiquitin monomer
1 2 3 4 5 6

Fig. 5B


Vector
His-SENP1
Sentrinized proteins
-p90
Sentrin-2 monomer-